SEQUENCE LISTING

<110> Kalchman, Michael
      Hayden, Michael R.
      Hackam, Abigail
      Chopra, Vikramjit
      Goldberg, Paul
      Nicholson, Donald W.
      Vaillancourt, John P.
      Rasper, Dita M.

<120> APOPTOSIS MODULATORS THAT INTERACT WITH
  THE HUNTINGTON'S DISEASE GENE

<130> MC010PI

<140> 09/701,205
<141> 2000-11-27

<150> PCT/US99/11743
<151> 1999-05-27

<150> 09/085,199
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gtggtggtga tccctgcaga ggcctcatcc cccgacagcg agccagtcct agagaaggat    240
gacctcatgg acatggatgc ctctcagcag aatttatttg acaacaagtt tgatgacntc    300
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gatgagaagg accacttaat tgagcgacta tacagagaga tcagtggatt gaaggcacag    420
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ttatctgctc ttcggaaaga actgcaggac actcagctca aactggccag cacagaggaa   1080
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<211> 386
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<213> Human

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            20                  25                  30
Lys Arg Val Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn Phe
        35                  40                  45
Leu Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val Ile
    50                  55                  60
Pro Ala Glu Ala Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys Asp
65                  70                  75                  80
Asp Leu Met Asp Met Asp Ala Glu Gln Gln Asn Leu Phe Asp Asn Lys
                85                  90                  95
Phe Asp Asp Phe Gly Ser Ser Ser Ser Asp Pro Phe Asn Phe Asn
            100                 105                 110
Ser Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile Glu Arg
    115                 120                 125
Leu Tyr Arg Glu Ile Ser Gly Leu Lys Ala Gln Leu Glu Asn Met Lys
    130                 135                 140
Thr Glu Ser Gln Arg Val Val Leu Gln Leu Lys Gly His Val Ser Glu
145                 150                 155                 160
Leu Glu Ala Asp Leu Ala Glu Gln Gln His Leu Arg Gln Gln Ala Ala
                165                 170                 175
Asp Asp Cys Glu Phe Leu Arg Ala Glu Leu Asp Glu Leu Arg Gln Arg
            180                 185                 190
Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Ser Glu Ile Glu Arg Lys
        195                 200                 205
Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu Lys Tyr Ser
    210                 215                 220
Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn Ala Glu Val
225                 230                 235                 240
Thr Lys Gln Val Ser Met Ala Arg Gln Ala Gln Val Asp Leu Glu Arg
                245                 250                 255
Glu Lys Lys Glu Leu Glu Asp Ser Leu Glu Arg Ile Ser Asp Gln Gly
            260                 265                 270
Gln Arg Lys Thr Gln Glu Gln Leu Glu Val Leu Glu Ser Leu Lys Gln
        275                 280                 285
Glu Leu Gly Thr Ser Gln Arg Glu Leu Gln Val Leu Gln Gly Ser Leu
    290                 295                 300
Glu Thr Ser Ala Gln Ser Glu Ala Asn Trp Ala Ala Glu Phe Ala Glu
305                 310                 315                 320
Leu Glu Lys Glu Arg Asp Ser Leu Val Ser Gly Ala Ala His Arg Glu
                325                 330                 335
Glu Glu Leu Ser Ala Leu Arg Lys Glu Leu Gln Asp Thr Gln Leu Lys
            340                 345                 350
Leu Ala Ser Thr Glu Glu Ser Met Cys Gln Leu Ala Lys Asp Gln Arg
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Asp Ala
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<211> 4796
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ccttntgttn tgttntcaac cgcctgcttc tgttttagca acgcagtgtt ttggtggaag     240
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ctttatgact acactgtcaa gcttctcttc aaactccact cctgcctccc agctgacacc     720
ctgcaaggcc accgggaccg cttcatggag cagtttacaa agttgaaaga tctgttctac     780
cgctccagca acctgcagtca cttcagacgg ctcattcaga tcccccagct gcctgagcac     840
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cctgcagagg cctcatccc cgacagcgag ccagtcctag agaaggatga cctcatggac     960
atggatgcct ctcagcagaa tttatttgac aacaagtttg atgacatctt tggcagttca    1020
ttcagcagtg atcccttcaa tttcaacagt caaatggtgt tgaacaagga tgagaaggac    1080
cacttaattg agcgactata cagagagatc agtggattga aggcacagct agaaaacatg    1140
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gatctggccg agcagcagca cctgcggcag caggcggccg acgactgtga attcctgcgg    1260
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tctgagatag aaaggaaagc tcaagccaat gaacagcgat atagcaagct aaaggagaag    1380
tacagcgagc tggttcagaa ccacgctgac ctgctgcgga agaatgcaga ggtgaccaaa    1440
caggtgtcca tggccagaca agcccaggta gatttggaac gagagaaaaa agagctggag    1500
gattcgttgg agcgcatcag tgaccagggc cagcggaaga ctcaagaaca gctggaagtt    1560
ctagagagct tgaagcagga acttggcaca agccaacggg agcttcaggt tctgcaaggc    1620
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gatcacctcc tctccacggt cacatccatt tccagctgca tcgagcaact ggagaaaagc    1980
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<212> PRT
<213> Human

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            20                  25                  30
Asn Pro Arg Phe Pro Gly Asn Leu Gln Met Ser Asp Arg Gln Leu Asp
        35                  40                  45
Glu Ala Gly Glu Ser Asp Val Asn Asn Phe Phe Gln Leu Thr Val Glu
    50                  55                  60
Met Phe Asp Tyr Leu Glu Cys Glu Leu Asn Leu Phe Gln Thr Val Phe
65                  70                  75                  80
Asn Ser Leu Asp Met Ser Arg Ser Val Ser Val Thr Ala Ala Gly Gln
                85                  90                  95
Cys Arg Leu Ala Pro Leu Ile Glu Val Ile Leu Arg Leu His Ser Leu Leu
            100                 105                 110
Tyr Asp Tyr Thr Val Lys Leu Leu Phe Lys Leu His Ser Cys Leu Pro
        115                 120                 125
Ala Asp Thr Leu Gln Gly His Arg Phe Asp Arg Phe Met Glu Gln Phe Thr
    130                 135                 140
Lys Leu Lys Asp Leu Phe Tyr Arg Ser Ser Asn Leu Gln Tyr Phe Lys
145                 150                 155                 160
Arg Leu Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn Pro Leu
                165                 170                 175
Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val Ile Pro
            180                 185                 190
Ala Glu Ala Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys Asp Asp
        195                 200                 205
Leu Met Asp Met Asp Ala Ser Gln Gln Asn Leu Phe Asp Asn Lys Phe
    210                 215                 220
Asp Asp Ile Phe Gly Ser Ser Phe Ser Ser Asp Pro Phe Asn Phe Asn
225                 230                 235                 240
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Ser Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile Glu Arg
            245                     250                     255
Leu Tyr Arg Glu Gln Ile Ser Gly Leu Lys Ala Gln Leu Glu Asn Met Lys
            260                     265                     270
Thr Glu Ser Gln Arg Val Val Leu Gln Leu Lys Gly His Val Ser Glu
            275                     280                     285
Leu Glu Ala Asp Leu Ala Glu Gln Gln His Leu Arg Gln Gln Gln Ala Ala
            290                     295                     300
Asp Asp Cys Glu Phe Leu Arg Ala Glu Leu Asp Glu Leu Arg Arg Gln
305                     310                     315                 320
Arg Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Ser Glu Ile Glu Arg
            325                     330                     335
Lys Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu Lys Tyr
            340                     345                     350
Ser Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn Ala Glu
            355                     360                     365
Val Thr Lys Gln Val Ser Met Ala Arg Gln Ala Gln Val Asp Leu Glu
370                     375                     380
Arg Glu Lys Lys Glu Leu Glu Asp Ser Leu Glu Arg Ile Ser Asp Gln
385                     390                     395                 400
Gly Gln Arg Lys Thr Gln Glu Gln Leu Glu Val Leu Glu Ser Leu Lys
            405                     410                     415
Gln Glu Leu Gly Thr Ser Gln Arg Gln Leu Gln Val Leu Gln Gly Ser
            420                     425                     430
Leu Glu Thr Ser Ala Gln Ser Glu Ala Asn Trp Ala Ala Glu Phe Ala
            435                     440                     445
Glu Leu Glu Lys Glu Arg Asp Ser Leu Val Ser Gly Ala Ala His Arg
            450                     455                     460
Glu Glu Glu Leu Ser Ala Leu Arg Lys Glu Leu Gln Asp Thr Gln Leu
465                     470                     475                 480
Lys Leu Ala Ser Thr Glu Glu Ser Met Cys Gln Leu Ala Lys Asp Gln
            485                     490                     495
Arg Lys Met Leu Leu Val Gly Ser Arg Lys Ala Ala Glu Gln Val Ile
            500                     505                     510
Gln Asp Ala Leu Asn Gln Leu Glu Glu Pro Pro Leu Ile Ser Cys Ala
            515                     520                     525
Gly Ser Ala Asp His Leu Leu Ser Thr Val Thr Ser Ile Ser Ser Cys
            530                     535                     540
Ile Glu Gln Leu Glu Lys Ser Trp Ser Gln Tyr Leu Ala Cys Pro Glu
545                     550                     555                 560
Asp Ile Ser Gly Leu Leu His Ser Ile Thr Leu Leu Ala His Leu Thr
            565                     570                     575
Ser Asp Ala Ile Ala His Gly Ala Thr Thr Cys Leu Arg Ala Pro Pro
            580                     585                     590
Glu Pro Ala Asp Ser Leu Thr Glu Ala Cys Lys Gln Tyr Gly Arg Glu
            595                     600                     605
Thr Leu Ala Tyr Leu Ala Ser Leu Glu Glu Glu Gly Ser Leu Glu Asn
            610                     615                     620
Ala Asp Ser Thr Ala Met Arg Asn Cys Leu Ser Lys Ile Lys Ala Ile
625                     630                     635                 640
Gly Glu Glu Leu Leu Pro Arg Gly Leu Asp Ile Lys Gln Glu Glu Leu
            645                     650                     655
Gly Asp Leu Val Asp Lys Glu Met Ala Ala Thr Ser Ala Ala Ile Glu
            660                     665                     670
Thr Cys Thr Ala Arg Ile Glu Glu Met Leu Ser Lys Ser Arg Ala Gly
            675                     680                     685
Asp Thr Gly Val Lys Leu Glu Val Asn Glu Arg Ile Leu Arg Cys Cys
            690                     695                     700
Thr Ser Leu Met Gln Ala Ile Gln Val Leu Ile Val Ala Ser Lys Asp
705                     710                     715                 720
Leu Gln Arg Glu Ile Val Glu Ser Gly Arg Gly Thr Ala Ser Pro Lys
            725                     730                     735
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- 5 -

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Glu Phe Tyr Ala Lys Asn Ser Arg Trp Thr Glu Gly Leu Ile Ser Ala
            740                 745                 750
Ser Lys Ala Val Gly Trp Gly Ala Thr Val Met Val Asp Ala Ala Asp
        755                 760                 765
Leu Val Val Gln Gly Arg Gly Lys Phe Glu Glu Leu Met Val Cys Ser
    770                 775                 780
His Glu Ile Ala Ala Ser Thr Ala Gln Leu Val Ala Ala Ser Lys Val
785                 790                 795                 800
Lys Ala Asp Lys Asp Ser Pro Asn Leu Ala Gln Leu Gln Gln Ala Ser
            805                 810                 815
Arg Gly Val Asn Gln Ala Thr Ala Gly Val Val Ala Ser Thr Ile Ser
        820                 825                 830
Gly Lys Ser Gln Ile Glu Glu Thr Asp Asn Met Asp Phe Ser Ser Met
    835                 840                 845
Thr Leu Thr Gln Ile Lys Arg Gln Glu Met Asp Ser Gln Val Arg Val
    850                 855                 860
Leu Glu Leu Glu Asn Glu Leu Gln Lys Glu Arg Gln Lys Leu Gly Glu
865                 870                 875                 880
Leu Arg Lys Lys His Tyr Glu Leu Ala Gly Val Ala Glu Gly Trp Glu
            885                 890                 895
Glu Gly Thr Glu Ala Ser Pro Pro Thr Leu Gln Glu Val Val Thr Glu
        900                 905                 910
Lys Glu
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<211> 1090
<212> PRT
<213> Human
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Thr Ala Asn Ala Arg Gln Trp Cys Pro Leu Pro Gln Asp Ala Gln Pro
            20                  25                  30
Ala Gly Ser Trp Glu Arg Cys Pro Pro Leu Pro Pro Ala Gly Arg Leu
        35                  40                  45
Gln Gly Thr Asp His Pro Trp Trp Gly Arg Leu Ala Gly Gly Gly
    50                  55                  60
Glu Arg Gly Gly Leu Trp Gly Gly Leu Ser His Ser Gln Arg Leu Ile
65                  70                  75                  80
His Leu Ile Leu Leu Ser Leu Pro Leu Leu Val Phe Gln Thr Val Ser
            85                  90                  95
Ile Asn Lys Ala Ile Asn Thr Gln Glu Val Ala Val Lys Glu Lys His
            100                 105                 110
Ala Arg Thr Cys Ile Leu Gly Thr His His Glu Lys Gly Ala Gln Thr
        115                 120                 125
Phe Trp Ser Val Val Asn Arg Leu Pro Leu Ser Ser Asn Ala Val Leu
    130                 135                 140
Cys Trp Lys Phe Cys His Val Phe His Lys Leu Leu Arg Asp Gly His
145                 150                 155                 160
Pro Asn Val Leu Lys Asp Ser Leu Arg Tyr Arg Asn Glu Leu Ser Asp
            165                 170                 175
Met Ser Arg Met Trp Gly His Leu Ser Glu Gly Tyr Gly Gln Leu Cys
        180                 185                 190
Ser Ile Tyr Leu Lys Leu Leu Arg Thr Lys Met Glu Tyr His Thr Lys
    195                 200                 205
Asn Pro Arg Phe Pro Gly Asn Leu Gln Met Ser Asp Arg Gln Leu Asp
    210                 215                 220
Glu Ala Gly Glu Ser Asp Val Asn Asn Phe Phe Gln Leu Thr Val Glu
225                 230                 235                 240
Met Phe Asp Tyr Leu Glu Cys Glu Leu Asn Leu Phe Gln Thr Val Phe
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- 6 -

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                      245                     250                     255
Asn Ser Leu Asp Met Ser Arg Ser Val Ser Val Thr Ala Ala Gly Gln
                  260                     265                     270
Cys Arg Leu Ala Pro Leu Ile Gln Val Ile Leu Asp Cys Ser His Leu
              275                     280                     285
Tyr Asp Tyr Thr Val Lys Leu Leu Phe Lys Leu His Ser Cys Leu Pro
290                     295                     300
Ala Asp Thr Leu Gln Gly His Arg Asp Arg Phe Met Glu Gln Phe Thr
305                     310                     315                     320
Lys Leu Lys Asp Leu Phe Tyr Arg Ser Ser Asn Leu Gln Tyr Phe Lys
                  325                     330                     335
Arg Leu Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn Phe Leu
              340                     345                     350
Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val Ile Pro
          355                     360                     365
Ala Glu Ala Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys Asp Asp
370                     375                     380
Leu Met Asp Met Asp Ala Ser Gln Asn Leu Phe Asp Asn Lys Phe
385                     390                     395                     400
Asp Asp Ile Phe Gly Val Ser Ser Phe Ser Ser Asp Pro Phe Asn Phe Asn
                  405                     410                     415
Ser Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile Glu Arg
              420                     425                     430
Leu Tyr Arg Glu Ile Ser Gly Leu Lys Ala Gln Leu Glu Asn Met Lys
          435                     440                     445
Thr Glu Ser Gln Arg Val Val Leu Gln Leu Lys Gly His Val Ser Glu
450                     455                     460
Leu Glu Ala Asp Leu Ala Glu Gln Gln His Leu Arg Gln Gln Ala Ala
465                     470                     475                     480
Asp Asp Cys Glu Phe Leu Arg Ala Glu Leu Asp Glu Leu Arg Arg Gln
              485                     490                     495
Arg Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Ser Glu Ile Glu Arg
          500                     505                     510
Lys Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu Lys Tyr
      515                     520                     525
Ser Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn Ala Glu
530                     535                     540
Val Thr Lys Gln Val Ser Met Ala Arg Gln Ala Gln Val Asp Leu Glu
545                     550                     555                     560
Arg Glu Lys Lys Glu Leu Glu Asp Ser Leu Glu Arg Ile Ser Asp Ser
                  565                     570                     575
Gly Gln Arg Lys Thr Gln Glu Gln Leu Glu Val Leu Glu Ser Leu Lys
              580                     585                     590
Gln Glu Leu Ala Thr Ser Gln Arg Glu Leu Gln Val Leu Gln Gly Ser
          595                     600                     605
Leu Glu Thr Ser Ala Gln Ser Glu Ala Asn Trp Ala Ala Glu Phe Ala
      610                     615                     620
Glu Leu Glu Lys Glu Arg Asp Ser Leu Val Ser Gly Ala Ala His Arg
625                     630                     635                     640
Glu Glu Glu Leu Ser Ala Leu Arg Lys Glu Leu Gln Asp Thr Gln Leu
                  645                     650                     655
Lys Leu Ala Ser Thr Glu Glu Ser Met Cys Gln Leu Ala Lys Asp Gln
              660                     665                     670
Arg Lys Met Leu Leu Val Gly Ser Arg Lys Ala Ala Glu Gln Val Ile
          675                     680                     685
Gln Asp Ala Leu Asn Gln Leu Glu Glu Pro Pro Leu Ile Ser Cys Ala
690                     695                     700
Gly Ser Ala Asp His Leu Leu Ser Thr Val Thr Ser Ile Ser Ser Cys
705                     710                     715                     720
Ile Glu Gln Leu Glu Lys Ser Trp Ser Gln Tyr Leu Ala Cys Pro Glu
              725                     730                     735
Asp Ile Ser Gly Leu His Ser Ile Thr Leu Leu Ala His Leu Thr
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                 740                     745                     750
Ser Asp Ala Ile Ala His Gly Ala Thr Thr Cys Leu Arg Ala Pro Pro
        755                     760                     765
Glu Pro Ala Asp Ser Leu Thr Glu Ala Cys Lys Gln Tyr Gly Arg Glu
770                     775                     780
Thr Leu Ala Tyr Leu Ala Ser Leu Glu Glu Glu Gly Ser Leu Glu Asn
785                     790                     795                     800
Ala Asp Ser Thr Ala Met Arg Asn Cys Leu Ser Lys Ile Lys Ala Ile
            805                     810                     815
Gly Glu Glu Leu Leu Pro Arg Gly Leu Asp Ile Lys Gln Glu Glu Leu
        820                     825                     830
Gly Asp Leu Val Asp Lys Glu Met Ala Ala Thr Ser Ala Ala Ile Glu
        835                     840                     845
Thr Ala Thr Ala Arg Ile Glu Glu Met Leu Ser Lys Ser Arg Ala Gly
850                     855                     860
Asp Thr Gly Val Lys Leu Glu Val Asn Glu Arg Ile Leu Gly Cys Cys
865                     870                     875                     880
Thr Ser Leu Met Gln Ala Ile Gln Val Leu Ile Val Ala Ser Lys Asp
            885                     890                     895
Leu Gln Arg Glu Ile Val Glu Ser Gly Arg Gly Thr Ala Ser Pro Lys
        900                     905                     910
Glu Phe Tyr Ala Lys Asn Ser Arg Trp Thr Glu Gly Leu Ile Ser Ala
        915                     920                     925
Ser Lys Ala Val Gly Trp Gly Ala Thr Val Met Val Asp Ala Ala Asp
930                     935                     940
Leu Val Val Gln Gly Arg Gly Lys Phe Glu Glu Leu Met Val Cys Ser
945                     950                     955                     960
His Glu Ile Ala Ala Ser Thr Ala Gln Leu Val Ala Ala Ser Lys Val
            965                     970                     975
Lys Ala Asp Lys Asp Ser Pro Asn Leu Ala Gln Leu Gln Gln Ala Ser
        980                     985                     990
Arg Gly Val Asn Gln Ala Thr Ala Gly Val Val Ala Ser Thr Ile Ser
        995                     1000                    1005
Gly Leu Ser Gln Ile Glu Glu Thr Asp Asn Met Asp Phe Ser Ser Met
    1010                    1015                    1020
Thr Leu Thr Gln Ile Lys Arg Gln Glu Met Asp Ser Gln Val Arg Val
1025                    1030                    1035                    1040
Leu Glu Leu Glu Asn Glu Leu Gln Lys Glu Arg Gln Lys Leu Gly Glu
                1045                    1050                    1055
Leu Arg Lys Lys His Tyr Glu Leu Ala Gly Val Ala Glu Gly Trp Glu
        1060                    1065                    1070
Glu Gly Thr Glu Ala Ser Pro Pro Thr Leu Gln Glu Val Val Thr Glu
    1075                    1080                    1085
Lys Glu
    1090
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<210> 6
<211> 3251
<212> DNA
<213> Human

<400> 6
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ccgccacgag ctggcccagc tgagggctgc ccagctggag cgcgagcgga gccagggcct     120
gcgtgaggag gctgagagga aggccagtgc cacggaggcg cgctacaaca agctgaagga     180
aaagcacagt gagctcgtcc atgtgcacgc ggagctgctc agaagaaacg cggacacagc     240
caagcagctg acggtgacgc agcaaagcca ggaggaggtg gcgcgggtga aggagcagct     300
ggccttccag gtggagcagg tgaagcggga gtcggagttg aagctagagg agaagagcga     360
ccagcaggag aagctcaaga gggagctgga ggccaaggcc ggagagctgg cccgcgcgca     420
ggaggccctg agccacacag agcagagcaa gtcggagctg agctcacggc tggacacact     480
gagtgcggag aaggatgctc tgagtggagc tgtgcggcag cgggaggcag acctgctggc     540
ggcgcagagc ctggtgcgcg agacagaggc ggcgctgagc cgggagcagc agccagcagc     600
```

```
ccaggagcag ggcgagttgc agggccggct ggcagagagg gagtctcagg agcaggggct    660
gcggcagagg ctgctggacg agcagttcgc agtgttggcg ggcgctggctc ccgaggaccg    720
gggcatcctg caggatgccg tgagcaagct ggacgacccc ctgcacctgc gctgtaccag    780
ctccccagac tacctggtga gcagggccca ggaggccttg gatgccgtga gcaccctgga    840
ggagggccac gcccagtacc tgacctcctt ggcagacgcc tccgccctgg tggcaggctct    900
gacccgcttc tcccacctgg ctgcggatac catcatcaat gggcgtgcca cctcgcacct    960
ggctcccacc accgctgccg accgcctcat agacaccgtc agggagtgcg gggcccgggc   1020
tctggagctc atggggcagc tgcaggacca gcaggctctg cggcacatgc aggccagcct   1080
ggtgcggaca ccctgccagg gcatccttca gctgggccaa gaactgaaac ccaagagcct   1140
agatgtgcgg caggaggagc tgggggccgt ggtcgacaag gagatggcgg ccacatccgc   1200
agccattgaa gatgctgtgc ggaggattga ggacatgatg aaccaggcac gccacgccag   1260
ctcgggggtg aagctggagg tgaacgagag gatcctcaac tcctgcacag acctgatgaa   1320
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ggtggtgctt cacacgggca agtatgagga gctcatcgtc tgctcccacg agatcgcagc   1560
cagcacggcc cagctggtgg cggcctccaa ggtgaaggcc aacaagcaca gcccccaccct   1620
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tggggcatca gcggaccctg gagaggaggt ggccatccgg ccccccgaag ccagctctgg   1920
tgtaaccacc aagaaccac ccctggccca gaagcccagc gtggccccca gacaggacca   1980
ccagcttgac aaaaaaggatg gcatctaccc agctcaactc gtgaactact aggcccccca   2040
ggggtccagc aggggtgctg gtgacaggcc tgggcctccg caactgccct gacaggaccg   2100
agaggccttg ccctccacc tggtgcccaa gcctcccgcc tcaccgtctg gatcaatgtc   2160
ctcaaggccc ctggcccta ctgagcctgc agggtcctgg gccatgtggg tggtgcttct   2220
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gggccagcgt ggggctccct gcctctctgga ctcctgaagg tcgtggatgg atggaaggca   2460
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ttttccaggca tcccggagagt gggctgggcc ctaggccctc cagctcagcc agaaaaagcc   2880
cagaaaccca ggtgctggac caggccctc agggagggac cctgcggcta gagtgggcta   2940
ggcctggct ttgcccgtca gatttgaacg aatgtgtgtc ccttgagccc aaggagagcg   3000
gcaggagggg tgggaccagg ctgggagga agagccagca gctgccatgc cctcctgctc   3060
ccccacccc agccctagcc ctttagcctt tcaccctgtg tctctggaaag gctaccaaat   3120
actggccaag gtcaggagga gcaaaaatga gccagcacca gcgccttggc tttgtgttag   3180
catttcctcc tgaagtgttc tgttggcaat aaaatgcact ttgactgtta aaaaaaaaa   3240
aaaaaaaaa a                                                        3251


<210> 7
<211> 676
<212> PRT
<213> Human

<400> 7
Gly Glu Leu Glu Glu Gln Arg Lys Gln Lys Gln Lys Ala Leu Val Asp
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Asn Glu Gln Leu Arg His Glu Leu Ala Gln Leu Arg Ala Ala Gln Leu
            20                  25                  30
Glu Arg Glu Arg Ser Gln Gly Leu Arg Glu Glu Ala Glu Arg Lys Ala
        35                  40                  45
Ser Ala Thr Glu Ala Arg Tyr Asn Lys Leu Lys Glu Lys His Ser Glu
    50                  55                  60
Leu Val His Val His Ala Glu Leu Leu Arg Lys Asn Ala Asp Thr Ala
65                  70                  75                  80
```

```
Lys Gln Leu Thr Val Thr Gln Gln Ser Gln Glu Glu Val Ala Arg Val
                 85                      90                      95
Lys Glu Gln Leu Ala Phe Gln Val Glu Gln Val Lys Arg Glu Ser Glu
                100                     105                     110
Leu Lys Leu Glu Glu Lys Ser Asp Gln Gln Glu Lys Leu Lys Arg Glu
        115                     120                     125
Leu Leu Ala Lys Ala Gly Glu Leu Ala Arg Ala Gln Glu Ala Leu Ser
    130                     135                     140
His Thr Glu Gln Ser Lys Ser Glu Leu Ser Ser Arg Leu Asp Thr Leu
145                     150                     155                     160
Ser Ala Glu Lys Asp Ala Leu Ser Gly Ala Val Arg Gln Arg Glu Ala
                165                     170                     175
Asp Leu Leu Ala Ala Gln Ser Leu Val Arg Glu Thr Glu Ala Ala Leu
            180                     185                     190
Ser Arg Glu Gln Gln Arg Ser Ser Gln Glu Gln Gly Glu Leu Gln Gly
    210                     200                     205
Arg Leu Ala Glu Arg Glu Ser Gln Glu Gln Gly Leu Arg Gln Arg Leu
    210                     215                     220
Leu Asp Glu Gln Phe Ala Val Leu Arg Gly Ala Ala Ala Glu Ala Ala
225                     230                     235                     240
Gly Ile Leu Gln Asp Ala Val Ser Lys Leu Asp Asp Pro Leu His Leu
                245                     250                     255
Arg Cys Thr Ser Ser Pro Asp Tyr Leu Val Ser Arg Ala Gln Glu Ala
            260                     265                     270
Leu Asp Ala Val Ser Thr Leu Glu Glu Gly His Ala Gln Tyr Leu Thr
        275                     280                     285
Ser Leu Ser Asp Ala Ser Ala Leu Val Ala Ala Leu Thr Arg Phe Ser
    290                     295                     300
His Leu Ala Ala Asp Thr Ile Ile Asn Gly Gly Ala Thr Ser His Leu
305                     310                     315                     320
Ala Pro Thr Asp Pro Ala Asp Arg Leu Ile Asp Thr Cys Arg Glu Cys
                325                     330                     335
Gly Ala Arg Ala Leu Glu Leu Met Gly Gln Leu Gln Asp Gln Gln Ala
            340                     345                     350
Leu Arg His Met Gln Ala Ser Leu Val Arg Thr Pro Leu Gln Gly Ile
    355                     360                     365
Leu Gln Leu Gly Gln Glu Leu Lys Pro Lys Ser Leu Asp Val Arg Gln
    370                     375                     380
Glu Glu Leu Gly Ala Val Val Asp Lys Glu Met Ala Ala Thr Ser Ala
385                     390                     395                     400
Ala Ile Glu Asp Ala Val Arg Arg Ile Glu Asp Met Met Asn Gln Ala
                405                     410                     415
Arg His Ala Ser Ser Gly Val Lys Leu Glu Glu Val Asn Glu Ile Leu
            420                     425                     430
Asn Ser Cys Thr Asp Leu Met Lys Ala Ile Arg Leu Leu Val Thr Thr
    435                     440                     445
Ser Thr Ser Leu Gln Lys Glu Ile Val Glu Ser Gly Arg Gly Ala Ala
    450                     455                     460
Thr Gln Gln Glu Phe Tyr Ala Lys Asn Ser Arg Trp Thr Glu Gly Leu
465                     470                     475                     480
Ile Ser Ala Ser Lys Ala Val Gly Trp Gly Ala Thr Gln Leu Val Glu
            485                     490                     495
Ala Ala Asp Lys Val Val Leu His Thr Gly Lys Tyr Glu Glu Leu Ile
        500                     505                     510
Val Cys Ser His Glu Ile Ala Ala Ser Thr Ala Gln Leu Val Ala Ala
    515                     520                     525
Ser Lys Val Lys Ala Asn Lys His Ser Pro His Leu Ser Arg Leu Gln
    530                     535                     540
Glu Cys Ser Arg Thr Val Asn Glu Arg Ala Ala Asn Val Val Ala Ser
545                     550                     555                     560
Thr Lys Ser Gly Gln Glu Gln Ile Glu Asp Arg Asp Thr Met Asp Phe
                565                     570                     575
```

- 10 -

```
Ser Gly Leu Ser Leu Ile Lys Leu Lys Lys Gln Glu Met Glu Thr Gln
            580                 585                 590
Val Arg Val Leu Glu Leu Glu Lys Thr Leu Glu Ala Glu Arg Met Arg
        595                 600                 605
Leu Gly Glu Leu Arg Lys Gln His Tyr Val Leu Ala Gly Ala Ser Gly
    610                 615                 620
Ser Pro Gly Glu Glu Val Ala Ile Arg Pro Ser Thr Ala Pro Arg Ser
625                 630                 635                 640
Val Thr Thr Lys Lys Pro Pro Leu Ala Gln Lys Pro Ser Val Ala Pro
                645                 650                 655
Arg Gln Asp His Gln Leu Asp Lys Lys Asp Gly Ile Tyr Pro Ala Gln
            660                 665                 670
Leu Val Asn Tyr
        675


<210> 8
<211> 2301
<212> DNA
<213> Mouse

<400> 8
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ctcggccctg tcagagcaca tcagtcctgt ggtggtgatc ccggcagagg tgtcatcccc    120
agacagtgag cctgtcctgg agaaggatga cctcatggac atggacgcct cccagcagac    180
tttgtttgac aacaagtttg atgacgtctt tggcagctca ttgagcagcg accctttcaa    240
tttcaacaat caaaatggcg tgaacaagga cgagaaggac cacttgattg aacgcctgta    300
cagagagatc agtggactga cagggcagct ggacaacatg aagattgaga gccagcgggc    360
catgctgcag ctgaagggtc gagtgagtga gctggaggca gagctagcag agcagcagca    420
cttgggccgg caggctatgg atgactgcga gttcctgcgc actgagctgg atgaactgaa    480
gaggcagcga gaggacacgg agaaggcaca gcgcagcctg actgagatag aagaaaggc     540
ccaggctaat gaacagaggt atagcaagtt aaaagaaag tacagtgaac tggtgcagaa    600
ccatgctgac ctgctgcgga agaacgcaga ggtgaccaaa caggtgtccg tggccggca     660
agcccaggtg gatttggaaa gagagaaaaa agagctagca gattcctttg cacgtgtaag    720
tgaccaggcc cagcggaaga ctcaagaca acaggatgtt ctagagaacc tgaagcatga    780
actggccacc agcagacagg agctgcaggt cctccacagc aacctggaaa cctctgccca    840
gtcagaggcg·aaatggctga cacagatcgc cgagttggag aaggaacaag gcagcttggc    900
gactgttgca gctcagagag aggaagagtt atcagccctc cgagaccagc tggaaagcac    960
ccagatcaag ctggctgggg cccagaatc catgtgccag caggagagg accagaggaa    1020
aaccctcttg gcagggatca ggaaggctgc ggagcgtgag atacaggagg cgctgagcca   1080
gcttgaggaa cccaccctca tcagctgtgc aggatccaca gatcaccttc tctccaaagt   1140
cagctccgtt tccagctgcc tcgagcaact ggaaaagaac ggcagccagt atctggcgtt   1200
cccagaagat attagtgagc ttctgcactc gatcaccctg cttgcccact tgaccggtga   1260
cactgtcatc caggggagtg ccaccagcct ccgggcccca ccggagccag ccgactcgtt   1320
gacggaggcc tgtaggcagt atggcagaga aaccctggcc tatctgtcct ccctggagga   1380
agaggaact ctgaggtcac agccttagg aattgctca gcagggtcaa    1440
gaccttggc gaggagctgc tgcccagggg cctggacatc aagcaggaag agctgggtga   1500
cctggtggaa aaggagatgg cagccacttc agctgccatt gaagctgcca ccacccggat   1560
agaggaaatt ctcagtaagt cccgagcagg agacacggga gtcaagctgg aggtgaatga   1620
gaggatcctg ggttcctgta ccagcctgat gcaggccatc aaggtgttcg ttgtggcctc   1680
caaggacctc cagaaggaga tagtggagag tggcagggt agtgcatccc ctaaagaatt   1740
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gggagctacc atcatggtgg atgctgctga tcttgtggtc caaggcaaag ggaagttcga   1860
ggagctgatg gtgtgttcac gcgagattgc tgccagtact gcccagctcg tggctgcatc   1920
caaggtgaaa gcgaacaagg gcagcctcaa tctgacccag ctgcagcagg cctctcgagg   1980
agtgaaccag gccacagccg ctgtggtggc ctcaaccatt tctgacaaat ctcagattga   2040
ggaaacagac agtatggact tctcaagcat gacactgacc cagatccagc gccaggagat   2100
ggattcccag gttaggggtgc tggagctgga aaatgacctg cagaaggagc gtcagaaact   2160
aggagagcta cggaagaaac actacgagct ggagggcgtg gctgaggggct gggaggaagg   2220
gacagaagca tcaccgtcta ctgtccaaga agcaataccg gacaaagagt agagccaagc   2280
cgacacccca cacatcagaa a                                           2301


<210> 9
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<211> 756
<212> PRT
<213> Mouse

<400> 9
Ala Arg Gly Leu Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn
1               5                   10                  15
Phe Leu Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val
            20                  25                  30
Ile Pro Ala Glu Val Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys
        35                  40                  45
Asp Asp Leu Met Asp Met Asp Ala Ser Gln Gln Thr Leu Phe Asp Asn
    50                  55                  60
Lys Phe Asp Asp Val Phe Gly Ser Ser Leu Ser Ser Asp Pro Phe Asn
65                  70                  75                  80
Phe Asn Asn Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile
                85                  90                  95
Glu Arg Leu Tyr Arg Glu Ile Ser Gly Leu Thr Gly Gln Leu Asp Asn
            100                 105                 110
Met Lys Ile Glu Ser Gln Arg Ala Met Leu Gln Leu Lys Gly Arg Val
        115                 120                 125
Ser Glu Leu Glu Ala Glu Leu Ala Glu Gln Gln His Leu Gly Arg Gln
    130                 135                 140
Ala Met Asp Asp Cys Glu Phe Leu Arg Thr Glu Leu Asp Glu Leu Lys
145                 150                 155                 160
Arg Gln Arg Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Thr Glu Ile
                165                 170                 175
Glu Arg Lys Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu
            180                 185                 190
Lys Tyr Ser Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn
        195                 200                 205
Ala Glu Val Thr Lys Gln Val Ser Val Ala Arg Gln Ala Gln Val Asp
    210                 215                 220
Leu Glu Arg Glu Lys Lys Glu Leu Ala Asp Ser Phe Ala Arg Val Ser
225                 230                 235                 240
Asp Gln Ala Gln Arg Lys Thr Gln Glu Gln Gln Asp Val Leu Glu Asn
                245                 250                 255
Leu Lys His Glu Leu Ala Thr Ser Arg Gln Glu Leu Gln Val Leu His
            260                 265                 270
Ser Asn Leu Glu Thr Ser Ala Gln Ser Glu Ala Lys Trp Leu Thr Gln
        275                 280                 285
Ile Ala Glu Leu Glu Lys Glu Gln Gly Ser Leu Ala Thr Val Ala Ala
    290                 295                 300
Gln Arg Glu Glu Glu Leu Ser Ala Leu Arg Asp Gln Leu Glu Ser Thr
305                 310                 315                 320
Gln Ile Lys Leu Ala Gly Ala Gln Glu Ser Met Cys Gln Gln Val Lys
                325                 330                 335
Asp Gln Arg Lys Thr Leu Leu Ala Gly Ile Arg Lys Ala Ala Glu Arg
            340                 345                 350
Glu Ile Glu Gln Glu Ala Leu Ser Gln Leu Glu Glu Pro Thr Leu Ile Ser
        355                 360                 365
Cys Ala Gly Ser Thr Asp His Leu Leu Ser Val Ser Ser Val Ser
370                 375                 380
Ser Cys Ser Leu Glu Gln Leu Gln Lys Asn Gly Ser Gln Tyr Leu Ala Cys
385                 390                 395                 400
Pro Glu Asp Ile Ser Gly Leu Leu His Ser Ile Thr Leu Leu Ala His
                405                 410                 415
Leu Thr Gly Asp Thr Val Ile Gln Gly Ser Ala Thr Ser Leu Arg Ala
            420                 425                 430
Pro Pro Glu Pro Ala Asp Ser Leu Thr Glu Ala Cys Arg Gln Tyr Gly
        435                 440                 445
Arg Glu Thr Leu Ala Tyr Leu Ser Glu Ser Leu Glu Glu Glu Gly Thr Val
```

```
          450                     455                     460
Glu Asn Ala Asp Val Thr Ala Leu Arg Asn Cys Leu Ser Arg Val Lys
465                     470                     475                     480
Thr Leu Gly Glu Glu Leu Leu Pro Arg Gly Leu Asp Ile Lys Gln Glu
                485                     490                     495
Glu Leu Gly Asp Leu Val Asp Lys Glu Met Ala Ala Thr Ser Ala Ala
                500                     505                     510
Ile Glu Ala Ala Thr Thr Arg Ile Glu Glu Ile Leu Ser Lys Ser Arg
        515                     520                     525
Ala Gly Asp Thr Gly Val Lys Leu Glu Val Asn Glu Arg Ile Leu Gly
                530                     535                     540
Ser Cys Thr Ser Leu Met Gln Ala Ile Lys Val Leu Val Val Ala Ser
545                     550                     555                     560
Lys Asp Leu Gln Lys Glu Ile Val Glu Ser Gly Arg Gly Ser Ala Ser
                565                     570                     575
Pro Lys Glu Phe Tyr Ala Lys Asn Ser Arg Trp Thr Glu Gly Leu Ile
                580                     585                     590
Ser Ala Ser Lys Ala Val Gly Trp Gly Ala Thr Ile Met Val Asp Ala
        595                     600                     605
Ala Asp Ala Leu Val Val Gln Gly Lys Gly Lys Phe Glu Glu Leu Met Val
610                     615                     620
Cys Ser Arg Glu Ile Ala Ala Ser Thr Ala Gln Leu Val Ala Ala Ser
                630                     635                     640
Lys Val Lys Ala Asn Lys Gly Ser Leu Asn Leu Thr Gln Leu Gln Gln
                645                     650                     655
Ala Ser Arg Gly Val Asn Gln Ala Thr Ala Ala Val Val Ala Ser Thr
                660                     665                     670
Ile Ser Gly Lys Ser Gln Ile Glu Glu Thr Asp Ser Met Asp Phe Ser
        675                     680                     685
Ser Met Thr Leu Thr Gln Ile Glu Lys Arg Gln Glu Met Asp Ser Gln Val
690                     695                     700
Arg Val Leu Glu Leu Glu Asn Asp Leu Gln Lys Glu Arg Gln Lys Leu
705                     710                     715                     720
Gly Glu Leu Arg Lys Lys His Tyr Glu Leu Glu Gly Val Ala Glu Gly
                725                     730                     735
Trp Glu Gly Thr Glu Ala Ser Pro Ser Thr Val Gln Glu Ala Ile
        740                     745                     750
Pro Asp Lys Glu
        755
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<210> 10
<211> 3979
<212> DNA
<213> Mouse
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<400> 10
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ggcgcgggtg ctgagccgca ggccggccca cagcctagag gccgagcgcg agcagttcga      180
caagacgcag gccatcagta tcagcaaagc catcaacagc caggaggccc cagtgaagga      240
gaagcatgcc cggcgtatca tcctgggcac gcatcatgag aagggagcct tcaccttctg      300
gtcctatgcc atcggcctgc cgctgtccag cagctccatc ctcagctgga agttctgtca      360
cgtccttcac aaggtcctcc gggacggaca cccaacagtc ctgcatgact atcagcggta      420
ccggagcaac atacgtgaga tcggtgactt gtggggccac cttcgtgacc agtatggaca      480
cctggtgaat atctatacca aactgttgct gactaagatc tcctccacc ttaagcaccc      540
ccagtttcct gcaggcctgg aggtaacaga tgaggtgttg gacgaaggcgg cgggaactga      600
tgtcaacaac attttcagc ttaccgtgga gatgtttgac tacatggact gtgaactgaa      660
gctttctgag tcagtttttcc ggcagctcaa cacggccatc gcagtgtccc agatgtcttc      720
tggccagtg cgcctagcgc cgctcatcca ggtccattca gactgcagcc acctgtacca      780
ctacacagtg aagctcatgt ttaagctgca ctcctgtctc ccggcagaca ccctgcaagg      840
ccacagggat cggttccacg agcagttcca cagcctcaaa aacttcttcc gccgggcttc      900
agacatgctg tacttcaaga ggctcatcca gatcccgcgg ctgcctgagg gaccccccaa      960
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tttcctgcgg gcttcagccc tggctgagca catcaagccg gtggtggtga ttcccgagga   1020
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ggagccagtg gtggtggctg acctctttga tcagaccttt ggacccccca atggctccat   1140
gaaggatgac agggacctcc aaatcgagaa cttgaagaga gaggtggaga ccctccgtgc   1200
tgagctggag aggattaaga tggaggcaca gcggtacatc tcccagctga agggccaggt   1260
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caacgagcag ctgcgccacg agctggccca gctcaaggcc ctgcagctgg agggcgcccg   1380
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cgcagacacg gccaagcagc tgacagtgac acagcagagc caggaggagg tggcacgggt   1560
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<211> 1068
<212> PRT
<213> Mouse

<400> 11
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Gly His Ser Leu Glu Ala Glu Arg Glu Gln Phe Asp Lys Thr Gln Ala
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Ile Ser Ile Ser Lys Ala Ile Asn Ser Gln Glu Ala Pro Val Lys Glu
        35                      40                  45
Lys His Ala Arg Arg Ile Ile Leu Gly Thr His His Glu Lys Gly Ala
    50                      55                  60
Phe Thr Phe Trp Ser Tyr Ala Ile Gly Leu Pro Leu Ser Ser Ser Ser
65                      70                  75                  80
Ile Leu Ser Trp Lys Phe Cys His Val Leu His Lys Val Leu Arg Asp
                85                  90                  95
Gly His Pro Asn Val Leu His Asp Tyr Gln Arg Tyr Arg Ser Asn Ile
            100                 105                 110
Arg Glu Ile Gly Asp Leu Trp Gly His Leu Arg Asp Gln Tyr Gly His
        115                 120                 125
Leu Val Asn Ile Tyr Thr Lys Leu Leu Leu Thr Lys Ile Ser Phe His
145                     150                 155                 160
Leu Lys His Pro Gln Phe Pro Ala Gly Leu Glu Val Thr Asp Glu Val
145                     150                 155                 160
Leu Glu Lys Ala Ala Gly Thr Asp Val Asn Asn Ile Phe Gln Leu Thr
            165                 170                 175
Val Glu Met Phe Asp Tyr Met Asp Cys Glu Leu Lys Leu Ser Glu Ser
            180                 185                 190
Val Phe Arg Gln Leu Asn Thr Ala Ile Ala Val Ser Gln Met Ser Ser
        195                 200                 205
Gly Gln Cys Arg Leu Ala Pro Leu Ile Gln Val Ile Gln Asp Cys Ser
        210                 215                 220
His Leu Tyr His Tyr Thr Val Lys Leu Met Phe Lys Leu His Ser Cys
225                     230                 235                 240
Leu Pro Ala Asp Thr Leu Gln Gly His Arg Asp Arg Phe His Glu Gln
            245                 250                 255
Phe His Ser Leu Lys Asn Phe Phe Arg Arg Ala Ser Asp Met Leu Tyr
            260                 265                 270
Phe Lys Arg Leu Ile Gln Ile Pro Arg Leu Pro Glu Gly Pro Pro Asn
        275                 280                 285
Phe Leu Arg Ala Ser Ala Leu Ala Glu His Ile Lys Pro Val Val Val
        290                 295                 300
Ile Pro Glu Glu Ala Pro Glu Glu Glu Pro Glu Asn Leu Ile Glu
305                     310                 315                 320
Ile Ser Ser Ala Pro Pro Ala Gly Glu Pro Val Val Val Ala Asp Leu
                325                 330                 335
Phe Asp Gln Thr Phe Gly Pro Pro Asn Gly Ser Met Lys Asp Asp Arg
            340                 345                 350
Asp Leu Gln Ile Glu Asn Leu Lys Arg Glu Val Glu Thr Leu Arg Ala
        355                 360                 365
Glu Leu Glu Lys Ile Lys Met Glu Glu Ala Glu Leu Arg Arg Tyr Ile Ser Glu Leu
        370                 375                 380
Lys Gly Leu Glu Val Asn Gly Leu Glu Ala Glu Leu Glu Glu Gln Arg Lys
385                     390                 395                 400
Gln Lys Gln Lys Ala Leu Glu Val Asp Asn Glu Gln Leu Arg His Glu Leu
            405                 410                 415
Ala Gln Leu Lys Ala Leu Gln Leu Glu Gly Ala Arg Asn Gln Gly Leu
        420                 425                 430
Arg Glu Glu Ala Glu Arg Lys Ala Ser Ala Thr Glu Ala Arg Tyr Ser
        435                 440                 445
Lys Leu Lys Glu Lys His Ser Glu Leu Ile Asn Thr His Ala Glu Leu
450                     455                 460
Leu Arg Lys Asn Ala Asp Thr Ala Lys Gln Leu Thr Val Thr Gln Gln
465                     470                 475                 480
Ser Gln Glu Glu Val Ala Arg Val Lys Glu Gln Leu Ala Phe Gln Met
            485                 490                 495
Glu Gln Ala Lys Arg Glu Ser Glu Met Lys Met Glu Glu Gln Ser Asp
            500                 505                 510
Gln Leu Glu Lys Leu Lys Arg Glu Leu Ala Ala Arg Ala Gly Glu Leu
        515                 520                 525
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Ala Arg Ala Gln Glu Ala Leu Ser Arg Thr Glu Gln Ser Gly Ser Glu
530                     535                 540
Leu Ser Ser Arg Leu Asp Thr Leu Asn Ala Glu Lys Glu Ala Leu Ser
545                 550                 555                 560
Gly Val Val Arg Gln Arg Glu Ala Glu Leu Leu Ala Ala Gln Ser Leu
            565                 570                 575
Val Arg Glu Lys Glu Glu Ala Leu Ser Gln Glu Gln Gln Arg Ser Ser
        580                 585                 590
Gln Glu Gly Lys Gly Glu Leu Arg Gly Gln Leu Ala Leu Lys Glu Ser Gln
        595                 600                 605
Glu Gln Gly Leu Arg Gln Lys Leu Leu Asp Glu Gln Leu Ala Val Leu
610                 615                 620
Arg Ser Ala Ala Ala Gly Glu Ala Ile Leu Leu Gln Asp Ala Val Ser
625                 630                 635                 640
Lys Leu Asp Asp Pro Leu His Leu Arg Cys Thr Ser Ser Pro Asp Tyr
                645                 650                 655
Leu Val Ser Arg Ala Gln Ala Ala Leu Asp Ser Val Ser Gly Leu Glu
        660                 665                 670
Gln Gly His Thr Gln Tyr Leu Ala Ser Ser Glu Asp Ala Ser Ala Leu
        675                 680                 685
Val Ala Ala Leu Thr Arg Phe Ser His Leu Ala Ala Asp Thr Ile Val
        690                 695                 700
Asn Gly Ala Ala Thr Ser His Leu Ala Pro Thr Asp Pro Ala Asp Arg
705                 710                 715                 720
Leu Met Asp Thr Cys Arg Glu Cys Gly Ala Arg Ala Leu Glu Leu Val
                725                 730                 735
Gly Gln Leu Gln Asp Gln Thr Val Leu Arg Arg Gln Ala Gln Pro Ser Leu
            740                 745                 750
Met Arg Ala Pro Leu Gln Gly Ile Leu Gln Leu Gly Gln Ser Leu Lys
            755                 760                 765
Pro Lys Ser Leu Asp Val Arg Gln Glu Glu Leu Gly Ala Met Val Asp
770                 775                 780
Lys Glu Met Ala Ala Thr Ser Ala Ala Ile Glu Asp Ala Val Arg Arg
785                 790                 795                 800
Ile Glu Asp Met Met Ser Gln Ala Arg His Glu Ser Ser Gly Val Lys
                805                 810                 815
Leu Glu Val Asn Glu Arg Ile Leu Asn Ser Cys Thr Asp Leu Met Lys
        820                 825                 830
Ala Ile Arg Leu Leu Val Met Thr Ser Thr Ser Leu Gln Lys Glu Ile
        835                 840                 845
Val Glu Ser Gly Arg Gly Ala Ala Thr Gln Gln Glu Phe Tyr Ala Lys
850                 855                 860
Asn Ser Arg Trp Thr Glu Gly Leu Ile Ser Ala Ser Lys Val Val Gly
865                 870                 875                 880
Trp Gly Ala Thr Gln Leu Val Glu Ser Ala Asp Lys Val Val Leu His
                885                 890                 895
Met Gly Lys Tyr Glu Glu Leu Ile Val Cys Ser His Glu Ile Ala Ala
            900                 905                 910
Ser Thr Ala Gln Leu Val Ala Ala Ser Lys Val Lys Ala Asn Lys Asn
        915                 920                 925
Ser Pro His Leu Ser Arg Leu Gln Glu Cys Ser Arg Thr Val Asn Glu
930                 935                 940
Arg Ala Ala Asn Val Val Ala Ser Thr Lys Ser Gly Gln Glu Gln Ile
945                 950                 955                 960
Glu Asp Arg Asp Thr Met Asp Phe Ser Gly Leu Ser Leu Ile Lys Leu
            965                 970                 975
Lys Lys Gln Glu Met Glu Thr Gln Val Arg Val Leu Glu Leu Glu Lys
        980                 985                 990
Thr Leu Glu Ala Glu Arg Val Arg Leu Gly Glu Leu Arg Lys Gln His
        995                 1000                1005
Tyr Val Leu Ala Gly Gly Met Gly Thr Pro Ser Glu Glu Glu Pro Ser
    1010                1015                1020
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Arg Pro Ser Pro Ala Pro Arg Ser Gly Ala Thr Lys Lys Pro Pro Leu
1025                1030                1035                1040
Ala Gln Lys Pro Ser Ile Ala Pro Arg Thr Asp Asn Gln Leu Asp Lys
                1045                1050                1055
Lys Asp Gly Val Tyr Pro Ala Gln Leu Val Asn Tyr
                1060                1065
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<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> sequencing primer

<400> 12
gaagataccc caccaaac                                              18

<210> 13
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA primer

<400> 13
gcttgacagt gtagtcataa aggtggctgc agtcc                           35

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 14
ggacatgtcc agggagttga atac                                       24

<210> 15
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 15
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<210> 16
<211> 516
<212> DNA
<213> Human

<400> 16
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gcatctcttt gtgcgggctt taattgccat gttgttgtgc caagggagtg agtggcggcg  180
ggaccagcag ctgggcacag ccaatgccag gcagtggtgc ccactccctc aggacgccca  240
gccagctggc tcctgggagc gctgcccacc tctgccccca gctgggcgcc tgcaaggaac  300
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      cgaccacccg tggggctggg ggaggttggc tggaggagga gaaaggggcg ggctctggga      360
      gggtctcagc cactctcaga ggcttattca tctcatcctc ctttccctcc ccttcttgt       420
      ttttcagact gtcagcatca ataaggccat taatacgcag gaagtggctg taaaggaaaa      480
      acacgccaga aatatccttt ggatgttgct tggaag                                516

<210> 17
<211> 193
<212> DNA
<213> Human

<400> 17
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      gaccttctgt tctgttgtca accgcctgcc tctgtctagc aacccagtgc tctgctggaa      120
      gttctgccat gtgttccaca aactcctccg agatggacac ccgaacgtga gttcctgggg      180
      ctatggggtg gca                                                         193

<210> 18
<211> 104
<212> DNA
<213> Human

<400> 18
      gtgttctttt gccctgcag gtcctgaagg actctctgag atacagaaat gaattgagtg        60
      acatgagcag gatgtgggtg agtttggaga tgtactcagg agcc                       104

<210> 19
<211> 327
<212> DNA
<213> Human

<400> 19
      aattcctggc tgcagatctc ttgactgtta tgttcttgtt gttgactctg tttccctcc        60
      tcttcctaaa agggcacct gagcgagggg tatggccagc tgtgcagcat ctacctgaaa       120
      ctgctaagaa ccaagatgga gtaccacacc aaagtgagtc tctgcggaca gttctgccgc      180
      caccgccgcc tcccctgctc catcccttca gccctccct gggctcattt gtcagctctt       240
      tcaggtaata gacagcccag gcttctgagg aagtgtgcac atcatgtacc caagctgtga      300
      gagaggaaag ccaccgccag gcccacg                                          327

<210> 20
<211> 331
<212> DNA
<213> Human

<400> 20
      gggctcaagc aatcctccca cctcggcctc ccaagtagct gggaccacag gcgtgtgcca        60
      ccacgcccgg ctgagagagg gctcttcatg tcttctgccc tgactccctt cctctgcctc      120
      cctccagaa tcccagttc ccaggcaacc tgcagtgag tgaccgccag ctggacgagg         180
      ctggagaag tgacgtgaac aacttgtaag tggctcctgc cctgagccca gggagggaga       240
      aagctttgt gaatgctgac acttctcata agggtcatgg agggcctgat gggggggaggc      300
      cgtggctggg atgggggacca aagcccctgg g                                    331

<210> 21
<211> 470
<212> DNA
<213> Human

<400> 21
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      acttggagct ggagttgtgt gtgtgtttgc gcatgcacat gagcattgga gactggagta      120
      gcgtagagcg tgggggaggg gacaggtaac agaccggcct caggctgtgg agtgtaagct      180
      ctctttcctc ttgggtccag tttccagtta acagtggaga tgtttgacta cctggagtgt      240
      gaactcaacc tcttccaaac aggtgagtct cttccctccc gtctaaccca ggctctcatg      300
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ggaactacct aattcctagt cctcctctcc ctgcaaagtg tgcagcacaa ggggtaggaa    360
aatggagaca ttcacacccc atctctggtc tctccaaccc tcgtgcaggg agggactgaa    420
cctcttcagt attttttcttt ttaagagaca aggtctcggc cgggtgcagt               470

<210> 22
<211> 565
<212> DNA
<213> Human

<400> 22
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tctgcccctc tgaagaggct gcctgtaatc ccctggctct accacctttc tccctcactt    180
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tgaggataaa agagcagggc ccaggcctttg gtgaccccag taaagcccct ggcttgccac   540
tcttgcgtcc agtgttacag gatct                                          565

<210> 23
<211> 233
<212> DNA
<213> Human

<400> 23
gggacagctc taggccagtc gtggccctg gcagtgctgg ccacatgccc cagggtagct      60
gggcccctcc ccctgagag cccgctgtg gcttccctgc cctctggtcc ccctcccctc      120
tcacactctt tccaatttct tccaggcctc ccagctgaca ccctgcaagg ccacggggac    180
cgcttcatgg agcagtttac aaagtaagtg gttcaagtaa caggaatgga ggt           233

<210> 24
<211> 578
<212> DNA
<213> Human

<400> 24
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ccctcaggtc cttctccacc cctaggttga aagatctgtt ctaccgctcc agcaacctgc    180
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ggagaccctg gccaaagccc attgactcta accaggtt                            578

<210> 25
<211> 390
<212> DNA
<213> Human

<400> 25
aaaaaaattt aaaaaattaa acaggtctga accgtttaat tcgagaaagg gggcattctc      60
ccatatcact caactgaccc acacacagaa ttctctggct ctctgactta ttctcactcc    120
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gggttggggg caatggctta tgcctgtaat                                     390
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<210> 26
<211> 547
<212> DNA
<213> Human

<400> 26
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cacggtagat ttgaatgtta aatttgcatc acactagcca ggacacagtgg ctcacacctg     360
taatcctagc actttgggag gccaaggcag gaggattacc tgaggtcgag agttcgagac     420
cagcctgggc aacagggtga aaccccgtc ttcaataaaa atgcaataat tagccgggtg     480
tgttggcagg cacctgtaat cccagctact cgggaagctg aggcatgaga attgcttgaa     540
cttggga                                                              547

<210> 27
<211> 436
<212> DNA
<213> Human

<400> 27
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aggggaatca ggtatttact tggaagcatg gtaggacccg cttctccggc ccatgcccgt     180
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tgggtggggg cggggg                                                    436

<210> 28
<211> 469
<212> DNA
<213> Human

<400> 28
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<210> 29
<211> 359
<212> DNA
<213> Human

<400> 29
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gcagaatgca gaggtgacca aacaggtgtc catggccaga caagcccagg tagatttgga     180
acgagagaaa aaagagctgg aggattcgtt ggagcgcatc agtgaccagg gccagcggaa     240
ggtgagtggg acgaggagca ctcgggaaat gagggaggg gctgttgagt tggtggcggg     300
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<210> 30
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<211> 209
<212> DNA
<213> Human

<400> 30
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agcaggaact tgccacaagc caacgggagc ttcaggttct gcaaggcagc ctggaaactt       180
ctgcccaggt aaatacctcc tttttttttt                                        209


<210> 31
<211> 485
<212> DNA
<213> Human

<400> 31
cccccactgc aatcagtgtg tccccgggag ggaatcagag tggcaggtta aagagccatc        60
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actcaaccag cgtctccctc tttccttgtg gtcacctttg cagtcagaag caaatcgggc       180
agccgagtcc gccgagctag agaaggagcg ggacagcctg gtgagtggcc cagctcatag       240
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cacagagggt cacggacatg gacacgagcg agcacctgtg aattcccacc gagggcctct       360
gcgcatgcac ggaggctggg aggaccccgg ggctgctgag aagggtttg gggccttggc       420
ctgattgtgc agacattctg taggtgtaat gccagcaggc cctgcattgc ctgcagagtc       480
catga                                                                   485


<210> 32
<211> 468
<212> DNA
<213> Human

<400> 32
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tagaatctat gtgccagctt gccaaagacc aacgaaaaat gcttctggtg gggtccagga       180
aggctgcgga gcaggtgata caagacgccc tgaaccagct tgaagaacct cctctcatca       240
gctgcgctgg gtctgcaggt acacttgcaa ttgcccagct ggcaggggc aggtccttac       300
agcctgagac tctgttgatg ttgaatccca tgtgagactt agctcagggg ctctcagccc       360
agcagcatgt cagcattacc ttaggggcgc ccaggcccca tcctagatca gttacatgtg       420
gaaactctgt gcattagtgc ctatacacta gtattttagt attttcctt                   468


<210> 33
<211> 393
<212> DNA
<213> Human

<400> 33
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tgctctgacc ttgccctgtg ttccctctca cagatcacct cctctccacg gtcacatcca       120
tttccagctg catcgagcaa ctggagaaaa gctggagcca gtatctggcc tgcccagaag       180
gtaagaatgg ccaaggacag tctctgtcgg ctagtgatgg ccagacaggg ttcagaagca       240
cctgaatgcg ggatagtgta caggtccctc tgcatcaaga aaggcatgta ggcaactcat       300
acaagaaagg catgtaggca actcataaaa cgggaggaga gggtatgaaa gtgtcaccat       360
caaccagacc tgagaaactt ctctttccaa tcc                                    393


<210> 34
<211> 421
<212> DNA
<213> Human

<400> 34
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aggggttcaga agcacctgaa tgcggggata gtgacaggtc cctctgcatc aagaaaggca      120
tgtaggcaac tcatcaaga aaggcatgta ggcaactcat aaaacgggag gagagggtat       180
gaaagtgtca ccatcaacca gacctgagaa acttctcttt ccaatcctgg cagacatcag       240
tggacttctc cattccataa ccctgctggc ccacttgacc agcgacgcca ttgctcatgg       300
tgccaccacc tgcctcagag ccccacctga gcctgccgac tgtgagtact ggggcatgag       360
gggctgttca tggaccaggg gagcaggggg cctttaaaag tctctgttgg gccgggcgca       420
g                                                                      421
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<210> 35
<211> 498
<212> DNA
<213> Human
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```
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cgccactgca ctccagcctg ggcaacaaga gcgagactcc atctcaaaaa aaaagtgtct       120
attgccttgt atctccagca ctgaccgagg cctgtaagca gtatggcagg gaaaccctcg       180
cctacctggc ctccctggag gaagagggaa gccttgagaa tgccgacagc acagccatga       240
ggaactgcct gagcaagatc aaggccatcg gcgaggtact tggagtagta tcattgagga       300
gcattgttat tcttctgggt gtgcgtgctg gtgaatggcc agggaatcgg tgatgttctg       360
agctagttct ttctgcactt agaacttgat tctagaaaga gattgttaaa attggaaaat       420
ctggccgggt gcagtgattt atgcgtgtaa tcccagcact ttgggaggcc gagtcaggag       480
gatcacttga ggctagac                                                    498
```

```
<210> 36
<211> 427
<212> DNA
<213> Human
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```
<400> 36
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tacagatggc agaggagaag agacaggagg cccaaggtc agttcagcct ttgtgatgtg        120
ttcacaggag ctcctgccca ggggactgga catcaagcag gaggagctgg gggacctggt       180
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aggaggttcc tgcaggatct cctgaaacga tgcctttgca gctgcccttc tgcaacactg       300
ctcattaaac atgtcacagt cgttcattaa ggccatggca accccctaag acagaaacca       360
gaatttgcca ggcacagtgg ctcatgcctg taacccagc accttgggag gatcacttga       420
gtccagg                                                                427
```

```
<210> 37
<211> 367
<212> DNA
<213> Human
```

```
<400> 37
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cttggggact tccagattca ggtttcccag ctaccacacg atgttggact gaaagtatag       120
taagacatca gtggatcctt aatattcaag gcacatttag aaaccatgct tcttttcac        180
aggagatgct cagcaaatcc cgagcaggag acacagggat caaattggag gtgaatgaaa       240
ggtcggtctg agcggcatgg tgggacctag gggagcagga tctgtcttcc tgacattggt       300
ctatactttg catacttatt agggaattag aggagagcag tagcagccac ggggaagggc       360
tgagttg                                                                367
```

```
<210> 38
<211> 502
<212> DNA
<213> Human
```

```
<400> 38
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tgcctttggc taggagtggg gaagagaacc gtcgtgttca ttgatcttgg atcttgatct       120
cagtgtatcc tcgacttgtt tgtttggcag gatccttggt tgctgtacca gcctcatgca       180
```

```
agctattcag gtgctcatcg tggcctctaa ggacctccag agagagattg tggagagcgg     240
cagggtgagc gtgggtgtgg gccctgggca ggaagaggag gcatcggtga cagactcccg     300
ctccaacgga ctctgtgatg ctgccgtctt actctgtgtg tccacctgag tacagagcag     360
ccactcctgt agatatcagc agaggccctg gggagaagtc agagctccag gacctcccca     420
gagggtggcc aggcatgtgt cccaactcca gctcccttcg cacaggcaga cattgttgga     480
acttgctgtg ggagccctt tt                                               502

<210> 39
<211> 437
<212> DNA
<213> Human

<400> 39
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gctcaataaa aggtggctat tactattttt tatttcccta gggtacagca tcccctaaag     180
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ctcttccatt gatccactcc aaacaatagc taaggaggga aaaaaaaatc tgtccccttag     360
aaataaacta ttgatcagga agtcaatagg accgagttta caagggagcc tggctctccc     420
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<210> 40
<211> 351
<212> DNA
<213> Human

<400> 40
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aaatttgagg agctaatggt gtgttctcat gaaattgctg ctagcacagc ccagcttgtg     240
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<210> 41
<211> 418
<212> DNA
<213> Human

<400> 41
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ctgtgatccc aaccaaatcc cacaggactg tgtctaaatt ctttcatatt tttcatct      418

<210> 42
<211> 279
<212> DNA
<213> Human

<400> 42
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acagatcaaa cgccaagaga tggattctca ggttaggggtg ctagagctag aaaatgaatt     180
gcagaaggag cgtcaaaaac tgggagagct tcggaaaaag cactacgagc ttgctggtgt     240
tgctgagggc tgggaagaag gtaagctgac tcaaaggat                            279

<210> 43
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```
<211> 3715
<212> DNA
<213> Human

<400> 43
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ctatctcgtg tgtgttattt ccccagccac aggccaaatc cttggagtcc caggggcagc     180
cacaccactg ccattaccca gtgccgagga catgcatgac acttcccaaa gactccctcc     240
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